We claim:

1. A method of ascertaining the susceptibility to PRRS infection in an animal comprising the steps of:

obtaining a sample of cellular material of known origin from said animal;

performing a CD 151 assay on said sample; and

using the results of said assay as a measure of the susceptibility of said animal.

2. The method of claim 1, said cellular material being selected from the group consisting of semen, blood, germplasm, ova, and sperm cells.

3. The method of claim 1, said assay step including the step of extracting the RNA from said sample.

4. The method of claim 3, further comprising the step of performing reverse-transcriptase PCR on said extracted RNA.

5. The method of claim 1, said assay step including the step of quantifying the amount of detected CD 151.

6. The method of claim 5, further including the step of comparing said quantified amount of CD 151 with a known standard for said cellular material sample.

7. The method of claim 6, said known standard representing the average susceptibility of said animal.

8. The method of claim 6, said known standard being determined by averaging a large number of quantified CD 151 amounts from cellular material samples of the same origin as said sample.

9. A method of comparing the PRRSV infection susceptibility of an animal to a known standard of PRRSV infection susceptibility, said known standard being correlated with a CD 151 level for cellular material of known origin, comprising the steps of:

obtaining a sample of cellular material of known origin from said animal;

analyzing said sample to determine the CD 151 level in said animal; and

comparing said determined CD 151 level from said sample with the CD 151 level of said known standard.

10. The method of claim 9, said known standard being from the same origin as said sample.

11. The method of claim 9, said analyzing step including the step of extracting the RNA from said sample.

12. The method of claim 11, further comprising the step of performing reverse-transcriptase PCR on said extracted RNA.

13. The method of claim 9, said analyzing step including the step of quantifying the amount of determined CD 151.

14. The method of claim 9, said sample comprising a cellular material sample selected from the group consisting of semen, ova, blood, germplasm, and sperm cells.

15. A method for determining if an animal is resistant to PRRSV infection comprising the steps of:

obtaining a sample of cellular material from said animal;

performing an assay for the presence of CD 151 in said sample; and

determining if said animal is resistant to PRRSV infection by the presence or absence of CD 151 in said sample.

16. The method of claim 15, said sample being of a known origin.

17. The method of claim 15, said sample being selected from the group consisting of semen, ova, blood, germplasm, and sperm cells.

18. A method of classifying PRRSV infection resistance in an animal comprising the steps of:

obtaining a sample of cellular material of known origin from said animal;

performing an assay on said sample to find the level of CD 151 in said sample;

comparing said CD 151 level of said sample with a known scale of CD 151, said known scale corresponding to a specific degree of PRRSV infection resistance; and

classifying said animal's PRRSV infection resistance based on said comparison with said scale.

19. The method of claim 18, said classification resulting in a percentile ranking of PRRSV infection resistance in said animal.

20. The method of claim 18, said sample being selected from the group consisting of blood, semen, ova, germplasm, and sperm sells.

21. The method of claim 18, said known scale being a scale for cellular material of the same origin as said sample.

22. The method of claim 18 wherein said known scales differ depending on the origin of said sample.

23. The method of claim 18, said assay step including the step of extracting the RNA from said sample.

24. The method of claim 23, further comprising the step of performing reverse-transcriptase PCR on said extracted RNA.

25. A method for detecting CD 151 in a sample of cellular material comprising the steps of:

extracting the RNA from said sample;

performing reverse-transcriptase PCR on said extracted RNA; and

analyzing said reverse-transcriptase PCR results for the presence of CD 151.

26. The method of claim 25, further comprising the step of quantifying the amount of CD 151.

27. The method of claim 25, said sample being of a known origin.

28. The method of claim 25, said sample being selected from the group consisting of semen, ova, blood, germplasm, and sperm cells.

29. A method of preparing PRRSV vaccine stock comprising the steps of:

providing a cell line;

transforming said cell line with CD 151;

infecting said cell line with PRRSV; and

causing said cell line to produce PRRSV progeny for use in said vaccine stock.

30. The method of claim 29, said cell line being of non-simian origin.

31. The method of claim 29, said cell line being non-susceptible to PRRSV infection prior to said transformation with CD 151.

32. The method of claim 29, said transforming step including stable transfection with a plasmid containing a CD 151 DNA sequence.

33. The method of claim 32, said CD 151 sequence having at least about 91% sequence homology with SEQ ID No. 1.

34. The method of claim 33, said CD 151 sequence having at least about 95% sequence homology with SEQ ID No. 1.

35. The method of claim 34, said CD 151 sequence having at least about 98% sequence homology with SEQ ID No. 1.

36. The method of claim 29, said CD 151 sequence being of non-simian origin.

37. The method of claim 36, said CD 151 sequence being of porcine origin.

38. The method of claim 32, said CD 151 sequence having at least 84% sequence homology with SEQ ID No. 14.

39. The method of claim 38, said CD 151 sequence having at least 90% sequence homology with SEQ ID No. 14.

40. The method of claim 39, said CD 151 sequence having at least 95% sequence homology with SEQ ID No. 14.

41. The method of claim 40, said CD 151 sequence having at least 98% sequence homology with SEQ ID No. 14.

42. The method of claim 29, said vaccine stock of said transformed cell line being of higher titer than was previously obtainable prior to transformation.

43. The method of claim 42, said titer of said transformed line being at least about 100 fold higher than was possible prior to transformation.

44. A transformed cell line containing DNA coding for CD 151, said cell line, prior to transformation, not containing DNA coding for CD 151.

45. The transformed cell line of claim 44, said cell line being of non-simian origin.

46. The transformed cell line of claim 44, said DNA coding for CD 151 being of non-simian origin.

47. The transformed cell line of claim 46, said DNA coding for CD 151 being of porcine origin.

48. An isolated DNA sequence having at least about 91% sequence homology with SEQ ID No. 1.

49. The DNA sequence of claim 48, said sequence having at least about 95% sequence homology with SEQ ID No. 1.

50. The DNA sequence of claim 49, said sequence having at least about 98% sequence homology with SEQ ID No. 1.

51. A plasmid containing a DNA sequence having at least about 91% sequence homology with SEQ ID No. 1.

52. The plasmid of claim 51, said plasmid containing a DNA sequence having at least about 95% sequence homology with SEQ ID No. 1.

53. The plasmid of claim 52, said plasmid containing a DNA sequence having at least about 98% sequence homology with SEQ ID No. 1.

54. A plasmid having the Genbank accession number AF 275666.

55. A plasmid containing a DNA sequence having at least 84% sequence homology with SEQ ID No. 14.

56. The plasmid of claim 55, said plasmid containing a DNA sequence having at least 90% sequence homology with SEQ ID No. 14.

57. The plasmid of claim 56, said plasmid containing a DNA sequence having at least 95% sequence homology with SEQ ID No. 14.

58. The plasmid of claim 57, said plasmid containing a DNA sequence having at least 98% sequence homology with SEQ ID No. 14.

59. A vector containing a DNA sequence having at least about 91% sequence homology with SEQ ID No. 1.

60. The vector of claim 59, said vector containing a DNA sequence having at least about 95% sequence homology with SEQ ID No. 1.

61. The vector of claim 60, said vector containing a DNA sequence having at least about 98% sequence homology with SEQ ID No. 1.

62. A vector containing a DNA sequence having at least 84% sequence homology with SEQ ID No. 14.

63. The vector of claim 62, said vector containing a DNA sequence having at least 90% sequence homology with SEQ ID No. 14.

64. The vector of claim 63, said vector containing a DNA sequence having at least 95% sequence homology with SEQ ID No. 14.

65. The vector of claim 64, said vector containing a DNA sequence having at least 98% sequence homology with SEQ ID No. 14.

66. A method of rendering a cell line susceptible to PRRSV infection comprising the step of transforming said cell line using a plasmid containing CD151 coding sequences.

67. The method of claim 66, said cell line being non-susceptible to PRRSV infection prior to said transforming step.

68. The method of claim 66, said cell line being of non-simian origin.

69. The method of claim 68, said cell line being of porcine origin.

70. The method of claim 66, said plasmid containing a sequence having at least about 91% sequence homology with SEQ ID No. 1.

71. The method of claim 70, said plasmid containing a sequence having at least about 95% sequence homology with SEQ ID No. 1.

72. The method of claim 71, said plasmid containing a sequence having at least about 98% sequence homology with SEQ ID No. 1.

73. The method of claim 66, said plasmid containing a sequence having the Genbank Accession No. AF 275666.

74. The method of claim 66, said plasmid containing a sequence having at least 84% sequence homology with SEQ ID No. 14.

75. The method of claim 74, said plasmid containing a sequence having at least 90% sequence homology with SEQ ID No. 14.

76. The method of claim 75, said plasmid containing a sequence having at least 95% sequence homology with SEQ ID No. 14.

77. The method of claim 76, said plasmid containing a sequence having at least 98% sequence homology with SEQ ID No. 14.

78. A method of selecting animals for breeding comprising the steps of:

screening a sample of cellular material from said animals for the presence of CD 151 to obtain a CD 151 level;

comparing said CD 151 level with a known standard related to CD 151 levels; and

selecting animals for breeding which had a CD 151 level lower than said known standard.

79. The method of claim 78, said sample being of known origin.

80. The method of claim 78, said sample being of the same origin as said known standard.

81. The method of claim 78, said CD 151 level being at least about 20% lower than said known standard.

82. The method of claim 81, said CD 151 level being at least about 35% lower than said known standard.

83. The method of claim 82, said CD 151 level being at least about 50% lower than said known standard.

84. The method of claim 78, said sample being selected from the group consisting of blood, semen, ova, germplasm, and sperm cells.

85. A method of modifying PRRSV production in cells which are susceptible to PRRSV infection comprising the step of transforming said cells with CD 151 .

86. The method of claim 85, said modifying resulting in an increased production of PRRSV in said cells.

87. The method of claim 85, said modifying resulting in the production of more PRRSV per milliliter of vaccine virus stock.

88. The method of claim 85, said CD 151 being of non-porcine origin.

89. The method of claim 88, said CD 151 being of porcine origin.

90. A method of blocking entry of PRRSV into cells comprising the step of blocking PRRSV viral RNA from interaction with CD 151.

91. The method of claim 90, said blocking step including contacting said cells with an anti-viral compound.

92. The method of claim 91, said anti-viral compound being selected from the group consisting of anti-RNA entry compounds.

93. The method of claim 92, said anti-viral compounds occupying binding sites on CD 151.

94. The method of claim 93, said anti-viral compounds having greater affinity for said binding sites than said PRRSV viral RNA.

95. The method of claim 93, said anti-viral compounds having greater avidity for said binding sites than said PRRSV viral RNA.

96. The method of claim 93, said anti-viral compounds being screened in a high throughput manner.

97. A method of diagnosing PRRSV infection in a swine herd comprising the steps of:

obtaining a sample of cellular material from an individual swine in said herd;

providing a CD 151 transformed cell line;

performing an *in vitro* diagnostic test using said sample and said transformed cell line; and

using the results of said diagnostic test to diagnose PRRSV infection.

98. The method of claim 97, said cellular material being selected from the group consisting of blood, semen, ova, germplasm, and sperm cells.

99. The method of claim 97, said diagnostic test being selected from the group consisting of virus isolation assays and immunodiagnostic assays.

100. The method of claim 99, said immunodiagnostic assays being selected from the group consisting of ELISA, indirect fluorescent antibody tests, and indirect immunoperoxidase tests.

101. The method of claim 97, said transformed cell line permitting greater virus replication than said cell line prior to transformation.

102. The method of claim 97, said cell line being of non-simian origin.

103. The method of claim 97, said transformed cell line including a CD 151 sequence of non-simian origin.

104. A method of integrating CD 151 coding sequences directly into a chromosome comprising the steps of:

providing a vector having CD 151 coding sequence therein;

contacting a chromosome with said vector; and

causing said CD 151 coding sequences to integrate with the chromosome.

105. The method of claim 104, said vector being a retro-viral vector.

106. The method of claim 104, further comprising the step of causing the expression of said coding sequences.

107. The method of claim 104, said CD 151 coding sequences being selected from the group consisting of simian CD 151 and porcine CD 151.

108. The method of claim 104, said CD 151 coding sequences having at least about 91% homology with SEQ ID No. 1.

109. The method of claim 108, said CD 151 coding sequences having at least about 95% homology with SEQ ID No. 1.

110. The method of claim 104, said CD 151 coding sequences having at least 84% sequence homology with SEQ ID No. 14.

111. The method of claim 110, said CD 151 coding sequences having at least 90% sequence homology with SEQ ID No. 14.

112. The method of claim 111, said CD 151 coding sequences having at least 95% homology with SEQ ID No. 14.

113. The method of claim 112, said CD 151 coding sequences having at least 98% sequence homology with SEQ ID No. 14.

114. A modified genome expressing an altered level of CD 151 in comparison to said genome prior to modification, said modification comprising an alteration in the number of CD 151 coding sequences in said genome.

115. An animal having the modified genome of claim 114.

116. An isolated mRNA sequence, said mRNA sequence corresponding to a DNA sequence having at least 84% sequence homology with SEQ ID No. 38.

117. The mRNA sequence of claim 116, said DNA sequence having at least 90% sequence homology with SEQ ID No. 38.

118. The mRNA sequence of claim 117, said DNA sequence having at least 95% sequence homology with SEQ ID No. 38.

119. The mRNA sequence of claim 118, said DNA sequence having at least 98% sequence homology with SEQ ID No. 38.

120. An isolated DNA sequence coding for CD 151, said DNA sequence having at least 84% sequence homology with SEQ ID No. 14.

121. The isolated DNA sequence of claim 120, said DNA sequence having at least 90% sequence homology with SEQ ID No. 14.

122. The isolated DNA sequence of claim 121, said DNA sequence having at least 95% sequence homology with SEQ ID No. 14.

123. The isolated DNA sequence of claim 122, said DNA sequence having at least 98% sequence homology with SEQ ID No. 14.

124. An isolated DNA sequence coding for CD 151, said sequence being derived from porcine CD 151.

125. The isolated DNA sequence of claim 124, said sequence comprising a sequence selected from the group consisting of SEQ ID Nos. 15-29.

126. The isolated DNA sequence of claim 125, said sequence including both introns and exons coding for CD 151.

127. The isolated DNA sequence of claim 126, at least one of said introns having at least 84% sequence homology with a sequence selected from the group consisting of SEQ ID Nos. 16, 18, 21, 23, 25, 27 and 29.

128. The isolated DNA sequence of claim 126, at least one of said exons having at least 84% sequence homology with a sequence selected from the group consisting of SEQ ID Nos. 15, 17, 19, 20, 22, 24, 26, and 28.

129. A vaccine for inducing effective immunity against PRRSV, said vaccine comprising viral progeny produced in a non-simian cell line transformed with non-simian CD 151.

130. The vaccine of claim 129, said CD 151 being of porcine origin.

131. The vaccine of claim 129, said CD 151 having at least 84% sequence homology with SEQ ID No. 14

132. A method of determining the effect of single nucleotide polymorphisms on PRRSV susceptibility comprising the steps of:

obtaining at least two CD 151 genomic sequences;

comparing single nucleotide polymorphisms between said sequences; and

correlating said single nucleotide polymorphisms with susceptibility to PRRSV.

133. A method of modulating viral RNA entry into cells comprising the step of altering the amount of CD 151 of said cells.

134. The method of claim 133, said RNA entry resulting from endocytosis.

135. The method of claim 133, said viral RNA being PRRSV RNA.

136. A method of comparing PRRSV susceptibility factors between individual swine, said method comprising the steps of:

obtaining the genetic sequence of at least two swine;

analyzing the amount of CD 151 encoding sequences; and

comparing the amount of CD 151 encoding sequences.

137. A method of determining CD 151 sequences of swine comprising the steps of:

taking a biopsy from a swine, said biopsy being taken from an ear notch or tail snip; and

performing PCR on said biopsy to determine CD 151 sequences.

138. The method of claim 137, including the step of using said determined CD 151 sequences and correlating expression levels with susceptibility to PRRSV.